

## **Supplementary Information**

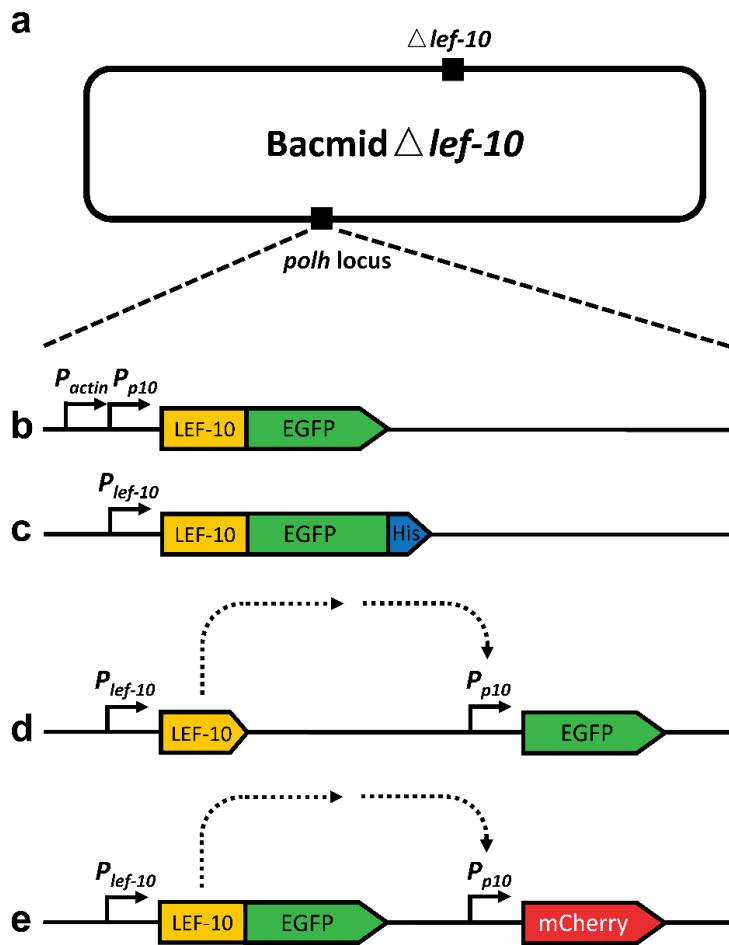
**A viral expression factor behaves as a prion**

Nan et al.

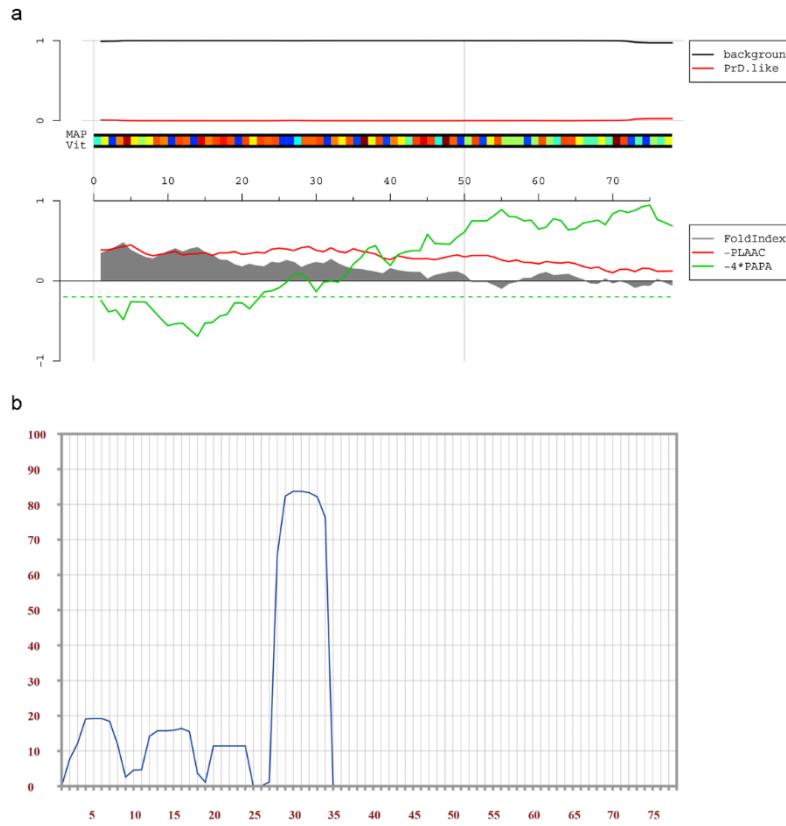
**This file includes:**

Supplementary Figure 1-9

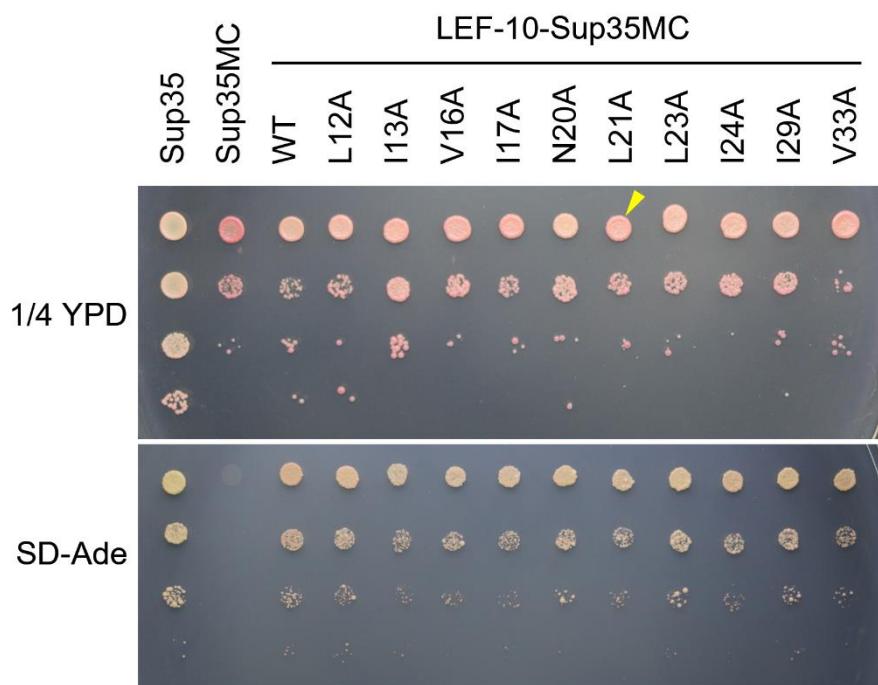
Supplementary Table 1-4



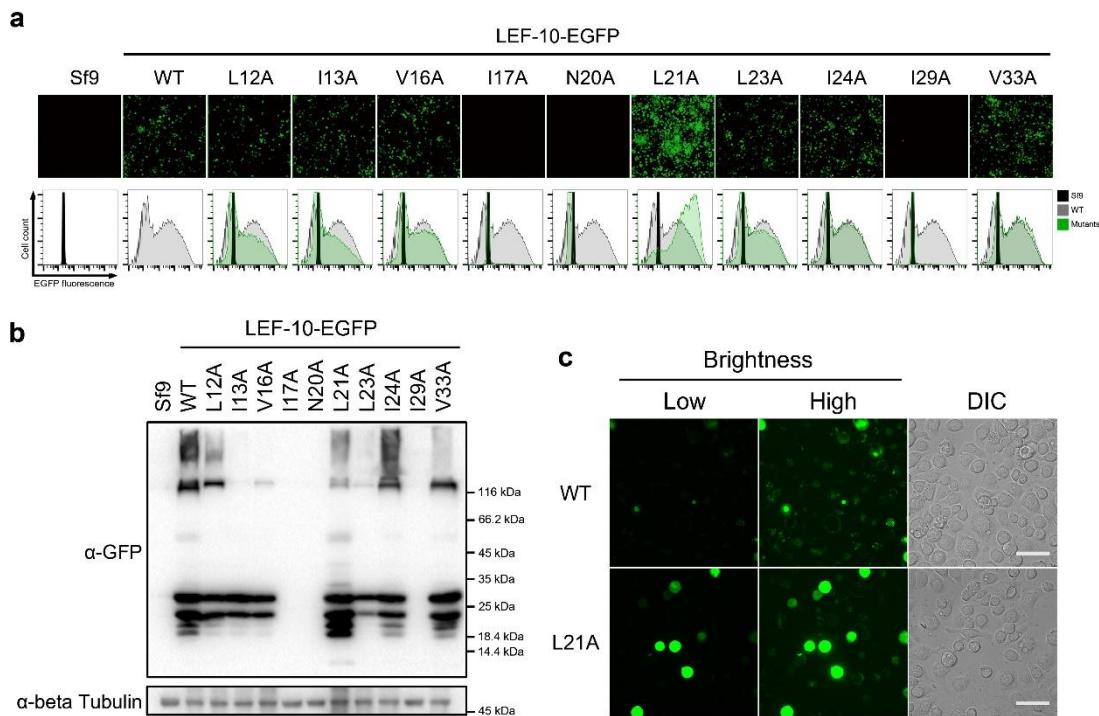
**Supplementary Figure 1** Diagram of generation of recombinant baculoviruses based on the *lef-10* knock-out Bacmid via homologous recombination. Homologous recombination occurs between the Bacmid $\Delta lef-10$  (**a**) and cassette fragments shown in **b**, **c**, **d** and **e**. **a** Bacmid $\Delta lef-10$  comprises a *polh* locus as the recombination site<sup>25</sup>. **b** LEF-10-EGFP was regulated by two tandem promoters. LEF-10-EGFP gene driven by *chicken actin* promoter could rescue Bacmid $\Delta lef-10$  as the promoter can drive the gene expression immediately after transfection or infection, and LEF-10-EGFP was over-expressed by the regulation of *p10* promoter (a strong promoter) in the late stage of infection. **c** LEF-10-EGFP gene driven by native *lef-10* promoter could rescue Bacmid $\Delta lef-10$ . **d** LEF-10 gene driven by its native promoter could rescue Bacmid $\Delta lef-10$ , and *p10* promoter driven EGFP could report the expression of baculovirus late gene. **e** LEF-10-EGFP gene driven by its native promoter could rescue Bacmid $\Delta lef-10$ , and *p10* promoter driven mCherry could report the expression of baculovirus late gene.



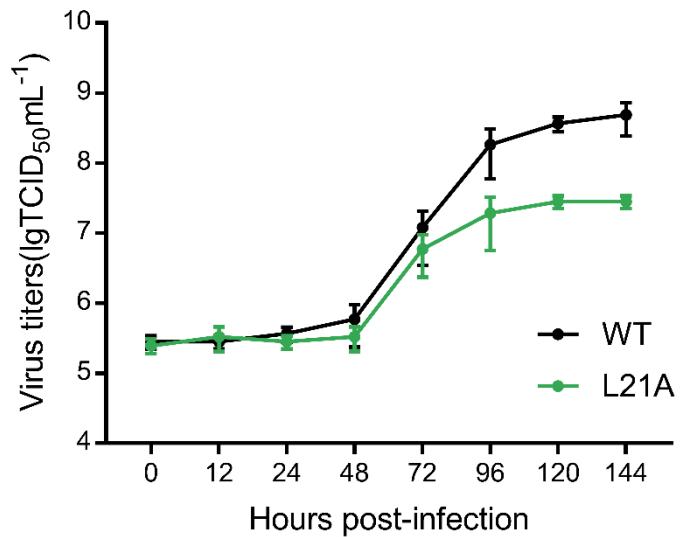
**Supplementary Figure 2** Computational analysis of LEF-10. **a** PLAAC prediction tools show that LEF-10 does not contain a prion-like domain. **b** The TANGO algorithm predicts that LEF-10 contains four aggregating regions, including three low probability regions and one high probability region.



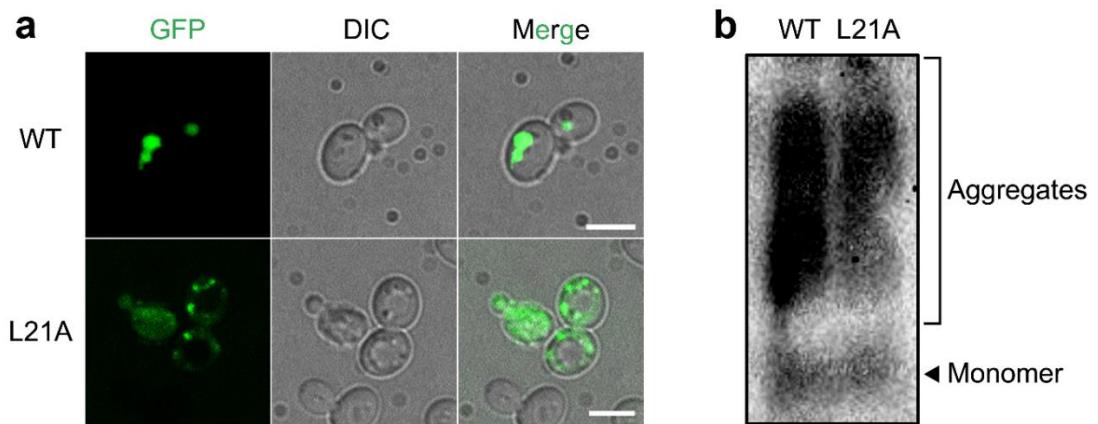
**Supplementary Figure 3** Alanine substitution assays for ten highly conserved amino acid residues in LEF-10 C1 region. Alanine substitution assays were performed to assess the role of the ten highly conserved amino acid residues in maintaining the LEF-10 prion properties. The strains harboring LEF-10-Sup35MC mutants showed varying degree of color change, from white to faint red. All strains growing on SD-Ade medium indicated the read-through of *ade1-14* premature stop codon, and the result suggested that the single alanine substitutions of these conserved amino acid residues in LEF-10 could not fully abolish the prion prone of LEF-10.



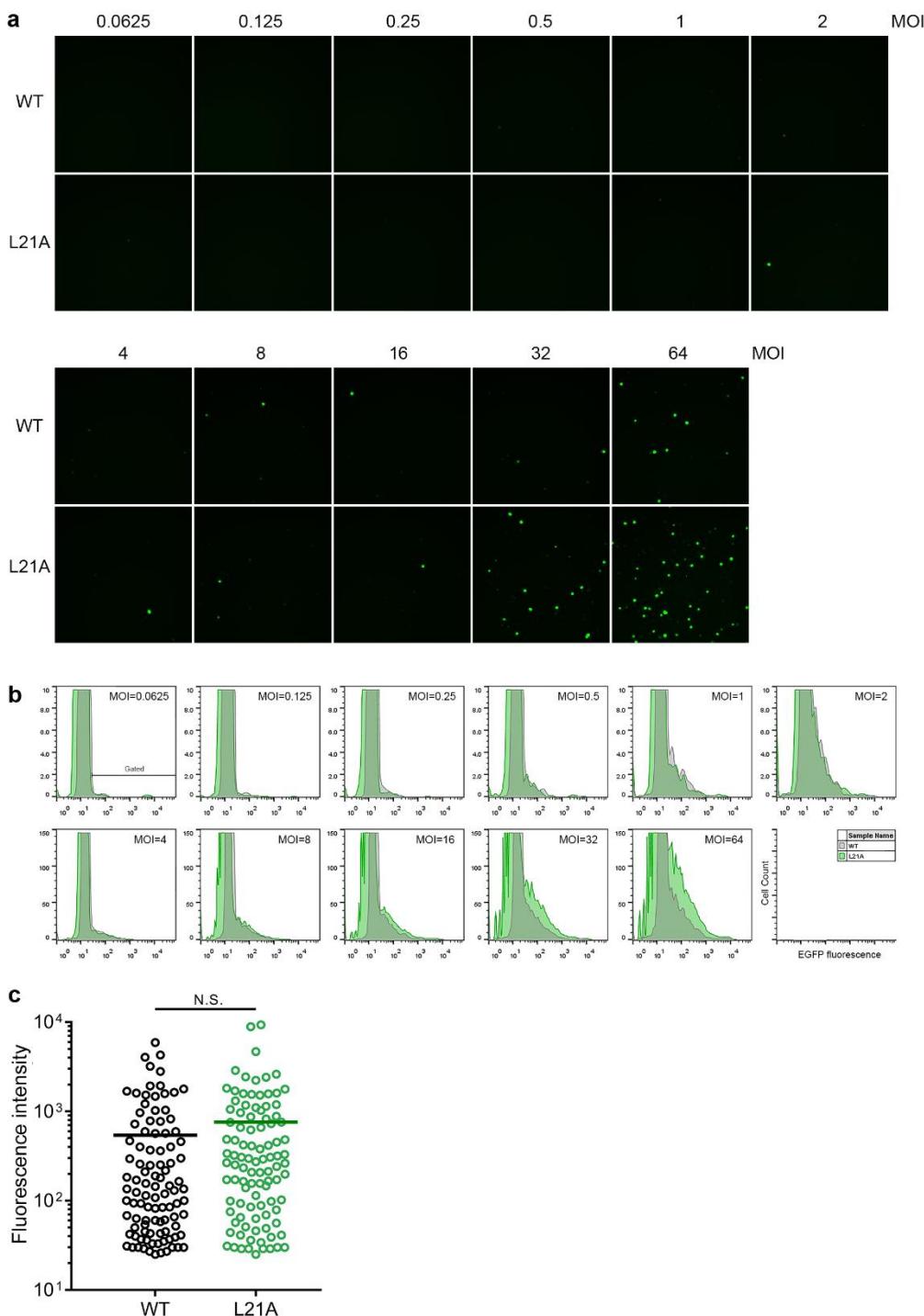
**Supplementary Figure 4** Virus rescue assays using over-expressed wild-type LEF-10 and LEF-10 mutants. Wild-type LEF-10 and 10 LEF-10 mutants fused with EGFP were driven by a tandem *actin/p10* promoter (Supplementary Fig. 1b). **a** Baculovirus-infected Sf9 cells were observed under a fluorescence microscope (top panel) and analyzed by flow cytometry (bottom panel) at 48 hpi. Among the LEF-10 mutants, LEF-10<sup>L21A</sup> displayed much higher activity than wild-type LEF-10, while three LEF-10 variants (LEF-10<sup>I17A</sup>, LEF-10<sup>N20A</sup> and LEF-10<sup>I29A</sup>) failed to rescue viruses. Other LEF-10 mutants showed similar activity with wild-type LEF-10 in the virus rescue assay. Uninfected Sf9 cells were examined as control. **b** Western blot analysis of baculovirus-infected Sf9 cells expressing LEF-10-EGFP chimeras. The protein levels detected by an anti-GFP antibody were consistent with their corresponding fluorescence intensity (**a**). The protein level of beta-tubulin in the cell lysates was determined as a loading control. **c** Laser confocal microscopy images of over-expressed LEF-10-EGFP and LEF-10<sup>L21A</sup>-EGFP in infected Sf9 cells at 48 hpi. Wild-type LEF-10-EGFP formed aggregates, whereas the LEF-10<sup>L21A</sup>-EGFP mutant is evenly distributed in baculovirus-infected Sf9 cells with low brightness. Non-diffuse fluorescence exhibited by LEF-10<sup>L21A</sup>-EGFP could be observed in some cells with high brightness. Scale bar, 50  $\mu$ m.



**Supplementary Figure 5** One-step growth curve of two recombinant viruses expressing LEF-10 and LEF-10<sup>L21A</sup>. Sf9 cells were infected with recombinant viruses expressing LEF-10 or LEF-10<sup>L21A</sup> at an MOI of 0.5. The virus titers were determined by a TCID<sub>50</sub> endpoint dilution assay. The virus titers were converted to log base 10. TCID<sub>50</sub>, 50% tissue culture infective dose. Data are represented as mean±SD from three replicates. Source data are provided as a Source Data file.

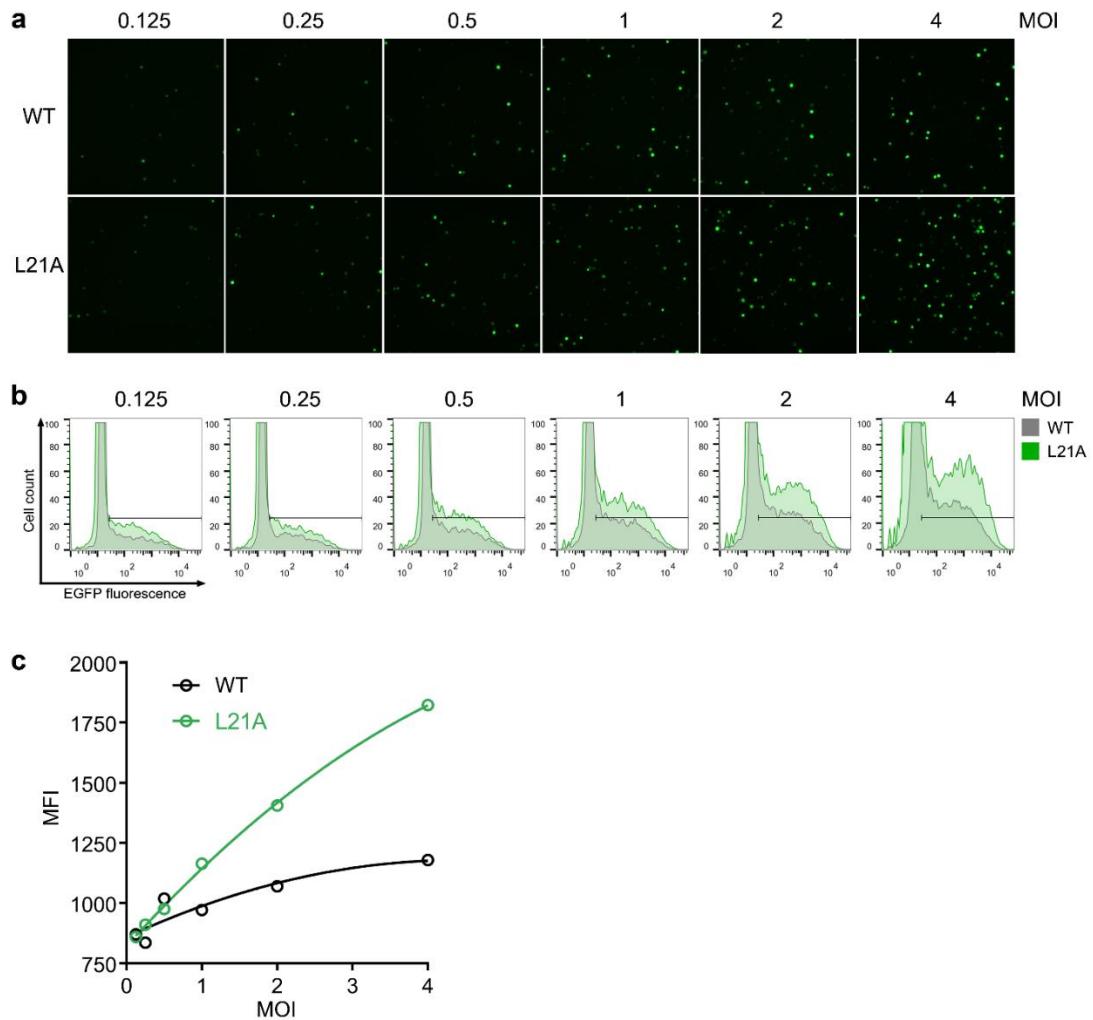


**Supplementary Figure 6** Characterization of GFP-tagged LEF-10 and GFP-tagged LEF-10<sup>L21A</sup> in yeast cells. **a** Laser confocal microscopy images displayed that LEF-10-GFP and LEF-10<sup>L21A</sup>-GFP fusion proteins exhibit different non-diffuse fluorescence patterns in yeast cell after 4 hours expression induced by 25  $\mu$ M CuSO<sub>4</sub>. LEF-10-GFP could form foci, whereas the LEF-10<sup>L21A</sup>-GFP formed punctate fluorescence pattern. Scale bar, 5  $\mu$ m. **b** SDD-AGE analysis of LEF-10-GFP and LEF-10<sup>L21A</sup>-GFP fusion proteins. The SDS-resistant aggregates could be detected in cell lysates of yeast strains containing LEF-10-GFP and LEF-10<sup>L21A</sup>-GFP fusion proteins using  $\alpha$ -GFP antibody.



**Supplementary Figure 7** Comparison of LEF-10-regulated late gene expression in infected Sf9 cells. Sf9 cells were infected with recombinant baculovirus encoding LEF-10 or LEF-10<sup>L21A</sup> under the control of native *lef-10* promoter. EGFP driven by *p10* promoter was detected as a reporter of late gene expression (Supplementary Fig. 1d). The sensor system functions by transmitting the aggregation state of LEF-10 to downstream gene reporter

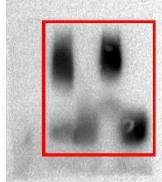
EGFP outputs. Two-fold dilutions of viruses at MOI of 0.0625, 0.125, 0.25, 0.5, 1.0, 2.0, 4.0, 8.0, 16.0, 32.0 and 64.0 were used for the *Sf9* cell infection. Infected cells were imaged and collected at 36 hpi. **a** Fluorescence images showed that the baculovirus late gene expression regulated by LEF-10 was at comparable levels with that regulated by LEF-10<sup>L21A</sup> at low MOIs (MOI≤8). However, following the protein expression increase at high MOIs, the late gene expression regulated by LEF-10 was significantly lower than the gene expression regulated by LEF-10<sup>L21A</sup>. **b** Flow cytometry analysis confirmed that baculovirus late gene expression regulated by LEF-10 was close to the gene expression levels regulated by LEF-10<sup>L21A</sup> at low MOIs (MOI≤8), but was much lower than that regulated by LEF-10<sup>L21A</sup> at high MOIs. **c** Fluorescence intensity of *p10* promoter-driven EGFP in 100 infected cells. 100 infected *Sf9* cells were gated (MOI≤1) and their EGFP fluorescence intensity was measured at 36 hpi using FlowJo® software. Bars represented mean. Two-tailed unpaired Student's *t*-test was performed (N.S., not significant). *P* value =0.2094.



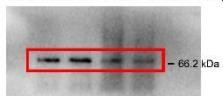
**Supplementary Figure 8** Comparison of mean fluorescence intensity (MFI) in infected *Sf9* cells. *Sf9* cells were infected with recombinant baculovirus encoding LEF-10 or LEF-10<sup>L21A</sup> under the control of the native *lef-10* promoter. EGFP driven by *p10* promoter was detected as a reporter of late gene expression (Supplementary Fig. 1d). Two-fold dilutions of viruses at MOI of 0.125, 0.25, 0.5, 1.0, 2.0 and 4.0 were used for the *Sf9* cell infection. Images were captured by fluorescence microscope (**a**) and cell samples were collected and analyzed by flow cytometry (**b, c**), at 60 hpi. **a** Fluorescence images showed that the baculovirus late gene expression regulated by LEF-10 was at comparable levels with that regulated by LEF-10<sup>L21A</sup> at low MOIs (MOI≤0.5). However, at high MOIs, the late gene expression regulated by LEF-10 was significantly lower than the gene expression regulated by

LEF-10<sup>L21A</sup>. **b, c** Flow cytometry analysis confirmed that baculovirus late gene expression regulated by LEF-10 was close to the gene expression levels regulated by LEF-10<sup>L21A</sup> at low MOIs, but was much lower than that regulated by LEF-10<sup>L21A</sup> at high MOIs. Cells were infected in parallel with a serial dilutions of viruses expressing wild-type LEF-10 or the LEF-10<sup>L21A</sup> mutant. In all samples, infected *Sf9* cells were gated and the mean fluorescence intensity (MFI) was calculated by FlowJo® software. Source data are provided as a Source Data file.

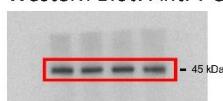
**Fig. 2b** upper  
SDD-AGE: Anti-Sup35C



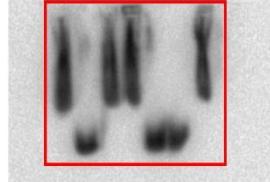
middle  
Western Blot: Anti-Sup35C



bottom  
Western Blot: Anti-PGK1



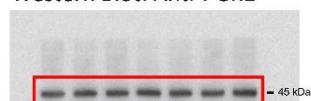
**Fig. 4b** upper  
SDD-AGE: Anti-Sup35C



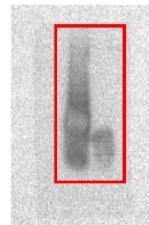
middle  
Western Blot: Anti-Sup35C



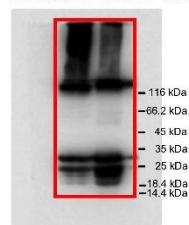
bottom  
Western Blot: Anti-PGK1



**Fig. 5g** SDD-AGE: Anti-His

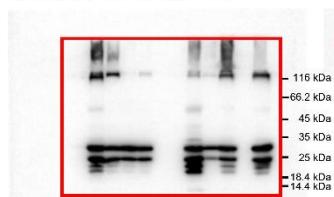


**Fig. 5h** Western Blot: Anti-His



**Supplementary Figure 4b**

upper  
Western Blot: Anti-GFP

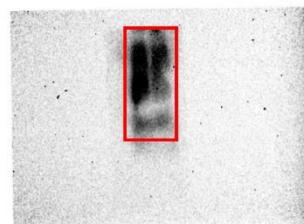


bottom  
Western Blot: Anti-β-tubulin



**Supplementary Figure 6b**

SDD-AGE: Anti-GFP



**Supplementary Figure 9** Uncropped scans of immunoblotting results. Red boxes highlight lanes used in figures.

**Supplementary Table 1** Plasmids used in this study.

Vectors Name	Plasmid Description	Source
pUKC1620	pRS313- <i>P<sub>sup35</sub></i> :Sup35	50
pUKC1620- $\Delta$ N	pRS313- <i>P<sub>sup35</sub></i> :Sup35MC	this study
pUKC1620-LEF-10	pRS313- <i>P<sub>sup35</sub></i> :LEF-10-Sup35MC	this study
pUKC1620-LEF-10 <sub>1-41</sub>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sub>1-41</sub> -Sup35MC	this study
pUKC1620-LEF-10 <sub>35-62</sub>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sub>35-62</sub> -Sup35MC	this study
pUKC1620-LEF-10 <sub>54-78</sub>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sub>54-78</sub> -Sup35MC	this study
pUKC1620-LEF-10 <sub>12-34</sub>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sub>12-34</sub> -Sup35MC	this study
pUKC1620-LEF-10 <sup>L12A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>L12A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>I13A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>I13A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>V16A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>V16A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>I17A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>I17A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>N20A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>N20A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>L21A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>L21A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>L23A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>L23A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>I24A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>I24A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>I29A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>I29A</sup> -Sup35MC	this study
pUKC1620-LEF-10 <sup>V33A</sup>	pRS313- <i>P<sub>sup35</sub></i> :LEF-10 <sup>V33A</sup> -Sup35MC	this study
p6431	pRS313- <i>P<sub>CUP1</sub></i> :GFP	S. L. L.
p6431-LEF-10	pRS313- <i>P<sub>CUP1</sub></i> :LEF-10-GFP	this study
p6431-LEF-10 <sup>L21A</sup>	pRS313- <i>P<sub>CUP1</sub></i> :LEF-10 <sup>L21A</sup> -GFP	this study
pTriEx-LEF-10-EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10-EGFP	this study
pTriEx-LEF-10 <sup>L12A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>L12A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>I13A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>I13A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>V16A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>V16A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>I17A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>I17A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>N20A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>N20A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>L21A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>L21A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>L23A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>L23A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>I24A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>I24A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>I29A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>I29A</sup> -EGFP	this study
pTriEx-LEF-10 <sup>V33A</sup> -EGFP	pTriEx- <i>P<sub>actin-p10</sub></i> :LEF-10 <sup>V33A</sup> -EGFP	this study
pTriEx- <i>P<sub>lef-10</sub></i> -LEF-10-EGFP	pTriEx- <i>P<sub>lef-10</sub></i> -LEF-10-EGFP-His	25
pTriEx- <i>P<sub>lef-10</sub></i> -LEF-10 <sup>L21A</sup> -EGFP	pTriEx- <i>P<sub>lef-10</sub></i> -LEF-10 <sup>L21A</sup> -EGFP-His	this study
pTriEx-EGFP	pTriEx- <i>P<sub>p10</sub></i> :EGFP	this study
pTriEx-LEF-10/EGFP	pTriEx- <i>P<sub>lef-10</sub></i> :LEF-10/ <i>P<sub>p10</sub></i> :EGFP	this study
pTriEx-LEF-10 <sup>L21A</sup> /EGFP	pTriEx- <i>P<sub>lef-10</sub></i> :LEF-10 <sup>L21A</sup> / <i>P<sub>p10</sub></i> :EGFP	this study
pTriEx-LEF-10-EGFP/mCherry	pTriEx- <i>P<sub>lef-10</sub></i> :LEF-10-EGFP/ <i>P<sub>p10</sub></i> :mCherry	25
pTriEx-LEF-10 <sup>L21A</sup> -EGFP/mCherry	pTriEx- <i>P<sub>lef-10</sub></i> :LEF-10 <sup>L21A</sup> -EGFP/ <i>P<sub>p10</sub></i> :mCherry	this study

**Supplementary Table 2** *Saccharomyces cerevisiae* strains used in this study.

Strains Name	Genotype	Construction
LJ14	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; p[SUP35-URA3]; [PSI<sup>+</sup>]</i>	50
LJ14-SUP1	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620; [PSI<sup>+</sup>]</i>	[ <i>PSI<sup>+</sup></i> ]; plasmid shuffle using LJ14
LJ14-SUP2	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620; [psi]</i>	[ <i>psi</i> ]
LJ14-SUP3	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-ΔN;</i>	plasmid shuffle using LJ14
LJ14-LEF1	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10; [PSI<sup>+</sup>]-like</i>	[ <i>PSI<sup>+</sup></i> ]-like; plasmid shuffle using LJ14
LJ14-LEF2	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10; [psi]-like</i>	[ <i>psi</i> ]-like; plasmid shuffle using LJ14
LJ14-LEF3	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sub>1-41</sub></i>	plasmid shuffle using LJ14
LJ14-LEF4	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sub>35-62</sub></i>	plasmid shuffle using LJ14
LJ14-LEF5	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sub>54-78</sub></i>	plasmid shuffle using LJ14
LJ14-LEF6	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sub>12-34</sub></i>	plasmid shuffle using LJ14
LJ14-LEF7	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>L12A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF8	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>L13A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF9	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>V16A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF10	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>I17A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF11	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>N20A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF12	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>L21A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF13	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>L23A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF14	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>I24A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF15	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>I29A</sup></i>	plasmid shuffle using LJ14
LJ14-LEF16	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i> <i>SUP35::loxP; pUKC1620-LEF-10<sup>V33A</sup></i>	plasmid shuffle using LJ14

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## Supplementary Table 2 (count.)

Strains Name	Genotype	Construction
LJ14-LEF17	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112; SUP35::loxP; hsp104::ura3; pUKC1620</i>	LJ14-SUP1 <i>hsp104::Ura3</i>
LJ14-LEF18	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112; SUP35::loxP; hsp104::ura3; pUKC1620-LEF-10</i>	LJ14-LEF1 <i>hsp104::Ura3</i>
LJ14-LEF19	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112; SUP35::loxP; hsp104::ura3; pUKC1620-LEF-10<sub>12-41</sub></i>	LJ14-LEF3 <i>hsp104::Ura3</i>
LJ14-LEF20	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112; SUP35::loxP; hsp104::ura3; pUKC1620-LEF-10<sub>12-34</sub></i>	LJ14-LEF6 <i>hsp104::Ura3</i>
LJ14-LEF-10-GF	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i>	LJ14-SUP1 transformed
P	<i>SUP35::loxP; pUKC1620; [PSI+]; p6431-LEF-10</i>	with p6431-LEF-10
LJ14-LEF-10 <sup>L21A</sup> -	<i>MATa ade1-14 trp1-289 his3Δ-200 ura3-52 leu2-3,112;</i>	LJ14-SUP1 transformed
GFP	<i>SUP35::loxP; pUKC1620; [PSI+]; p6431-LEF-10<sup>L21A</sup></i>	with p6431-LEF-10 <sup>L21A</sup>

**Supplementary Table 3** Viruses used in this study.

Virus Name	Target Encoding Proteins	Source
vAc/ <i>Plef-10</i> :LEF-10-EGFP- <i>P<sub>p10</sub></i> :mCheerry	LEF-10-EGFP and mCherry as the late gene reporter	25
vAc/ <i>Plef-10</i> :LEF-10L21A-EGFP- <i>P<sub>p10</sub></i> :mCherry	LEF-10 <sup>L21A</sup> -EGFP and mCherry as the late gene reporter	this study
vAc/ <i>Actin-p10</i> :LEF-10-EGFP	over-expressed LEF-10-EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>L12A</sup> -EGFP	over-expressed LEF-10 <sup>L12A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>I13A</sup> -EGFP	over-expressed LEF-10 <sup>I13A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>V16A</sup> -EGFP	over-expressed LEF-10 <sup>V16A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>I17A</sup> -EGFP	over-expressed LEF-10 <sup>I17A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>N20A</sup> -EGFP	over-expressed LEF-10 <sup>N20A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>L21A</sup> -EGFP	over-expressed LEF-10 <sup>L21A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>L23A</sup> -EGFP	over-expressed LEF-10 <sup>L23A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>I24A</sup> -EGFP	over-expressed LEF-10 <sup>I24A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>I29A</sup> -EGFP	over-expressed LEF-10 <sup>I29A</sup> -EGFP	this study
vAc/ <i>Actin-p10</i> :LEF-10 <sup>V33A</sup> -EGFP	over-expressed LEF-10 <sup>V33A</sup> -EGFP	this study
vAc/ <i>Plef-10</i> :LEF-10-EGFP	LEF-10-EGFP-His	25
vAc/ <i>Plef-10</i> :LEF-10 <sup>L21A</sup> -EGFP	LEF-10 <sup>L21A</sup> -EGFP-His	this study
vAc/ <i>Plef-10</i> :LEF-10- <i>P<sub>p10</sub></i> :EGFP	LEF-10 and EGFP as the late gene reporter	this study
vAc/ <i>Plef-10</i> :LEF-10 <sup>L21A</sup> - <i>P<sub>p10</sub></i> :EGFP	LEF-10 <sup>L21A</sup> and EGFP as the late gene reporter	this study

**Supplementary Table 4** Primers used in this study.

Primer Name	Sequences (5'-3')
SUPMC-FA	tcaaaactctagatctgaattcatgtcttgaacgact
SUPMC-FB	aacatctatatcgccactagcaacaatgcggattcaaactctagatctgaattc
SUPMC-FC	aacaggatcttcatcgactgctcggaaaataacatctatctgccactag
SUPMC-RABC	gcggggactctataattggagaggtgaag
LEF-10-1F	agcctctagaacgaacgtatggtc
LEF-10-35F	gccgtcttagagaccaagaaccgtatcaag
LEF-10-54F	attatctagaaccgtatgcggccgccaag
LEF-10-41R	cggcgaattcaactgtatcggtttcttg
LEF-10-62R	tacggaaattctgcacgcgttggcggc
LEF-10-78R	tagagaattccgtggacgcgttactttt
LEF-10-L12A_Fm	gcgacggacgtcaacgcgttatcaatttgtactg
LEF-10-L12A_Rm	cagtacacaattgtatgcgttgacgtccgtcg
LEF-10-I13A_Fm	acggacgtcaacctggctaatttgtactgaa
LEF-10-I13A_Rm	ttcagtacacaatttagccagggtacgtccg
LEF-10-V16A_Fm	aacctgatcaatttgtctgtactgaaagataatttat
LEF-10-V16A_Rm	taaattatcttcagagcacaattgtatcggtt
LEF-10-L17A_Fm	ctgatcaatttgttagctaaagataattttt
LEF-10-L17A_Rm	aaataaaattatctttagctacacaattgtatcg
LEF-10-N20A_Fm	tgtgtactgaaagatgcctttttgtatagat
LEF-10-N20A_Rm	atctatcaaaaaataagcatcttcagtagacaca
LEF-10-L21A_Fm	gtactgaaagataatgcctttttgtatagataat
LEF-10-L21A_Rm	attatctatcaaaaaagcattatcttcagtagacac
LEF-10-L23A_Fm	aaagataattttgtatagataataattac
LEF-10-L23A_Rm	gtaattattatctatagcaaataaaattatcttcag
LEF-10-I24A_Fm	gataattttttggctgataataattacatt
LEF-10-I24A_Rm	aatgttaattttatcagccaaaaataattatc
LEF-10-I29A_Fm	atagataataattacgctatttaatgtgttc
LEF-10-I29A_Rm	gaacacattaaaatagcgttaattttatcta
LEF-10-V33A_Fm	tacattatttaaatgcgttgcaccaagaaacc
LEF-10-V33A_Rm	ggtttcttggcgttgcaccaagcattaaaataatgt
LEF-10-C1F	agcctctagaacgaacgtatggtc
LEF-10-C3R	tagagaattccgtggacgcgttactttt
Del-test-F	attgaaacctccatcggttag
hsp104-test-R	ggaacaagtgcacaaaggaacg
URA3-test-R	gaaaagctgtgtatggcgcac
DeIHSP104-F	ggcaaaggggcgcaaacttatgcacactgcccagattattataaggcgagcagatgtactgagagt gcacc
DeIHSP104-R	caatttccatactgtccctattatcgcatcacctaactgtcagccattttgtctggccgcattcttc
LEF10-F (y)	ccggccaccgcggatggctagcacgaacgtatggcgcac
LEF10-R (y)	gagttcttccttgctagccgtggacgcgttactttgc
Sup35-F	ccggccaccgcggatggctagtcggattcaaaccaggcaa

## **Supplementary Table 4 (count.)**